S. Gucker

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information                    ENTERED
 4
 5          (i) APPLICANT: Hillman, Jennifer L.
 6                         Lal, Preeti
 7                         Tang, Y. Tom
 8                         Yue, Henry
 9                         Corley, Neil C.
10
11          (ii) TITLE OF THE INVENTION: KINESIN LIGHT CHAIN HOMOLOG
12
13          (iii) NUMBER OF SEQUENCES: 3
14
15          (iv) CORRESPONDENCE ADDRESS:
16             (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
17             (B) STREET: 3174 Porter Dr.
18             (C) CITY: Palo Alto
19             (D) STATE: CA
20             (E) COUNTRY: USA
21             (F) ZIP: 94304
22
23          (v) COMPUTER READABLE FORM:
24             (A) MEDIUM TYPE: Diskette
25             (B) COMPUTER: IBM Compatible
26             (C) OPERATING SYSTEM: DOS
27             (D) SOFTWARE: FastSEQ for Windows Version 2.0
28
29          (vi) CURRENT APPLICATION DATA:
30             (A) APPLICATION NUMBER: To Be Assigned
31             (B) FILING DATE: Filed Herewith
32
33          (vii) PRIOR APPLICATION DATA:
34             (A) APPLICATION NUMBER:
35             (B) FILING DATE:
36
37          (viii) ATTORNEY/AGENT INFORMATION:
38             (A) NAME: Billings, Lucy J.
39             (B) REGISTRATION NUMBER: 36,749
40             (C) REFERENCE/DOCKET NUMBER: PF-0484 US
41
42          (ix) TELECOMMUNICATION INFORMATION:
43             (A) TELEPHONE: 650-855-0555
44             (B) TELEFAX: 650-845-4166
45
46             (2) INFORMATION FOR SEQ ID NO:1:
```

```
47
48            (i) SEQUENCE CHARACTERISTICS:
49               (A) LENGTH: 619 amino acids
50               (B) TYPE: amino acid
51               (C) STRANDEDNESS: single
52               (D) TOPOLOGY: linear
53
54           (vii) IMMEDIATE SOURCE:
55               (A) LIBRARY: SMCANOT01
56               (B) CLONE: 2479739
57
58           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60     Met Ser Gly Leu Val Leu Gly Gln Arg Asp Glu Pro Ala Gly His Arg
61      1               5                  10                  15
62     Leu Ser Gln Glu Glu Ile Leu Gly Ser Thr Arg Leu Val Ser Gln Gly
63                    20                  25                  30
64     Leu Glu Ala Leu Arg Ser Glu His Gln Ala Val Leu Gln Ser Leu Ser
65                 35                  40                  45
66     Gln Thr Ile Glu Cys Leu Gln Gln Gly Gly His Glu Glu Gly Leu Val
67        50                  55                  60
68     His Glu Lys Ala Arg Gln Leu Arg Arg Ser Met Glu Asn Ile Glu Leu
69     65                  70                  75                  80
70     Gly Leu Ser Glu Ala Gln Val Met Leu Ala Leu Ala Ser His Leu Ser
71                 85                  90                  95
72     Thr Val Glu Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu
73                100                 105                 110
74     Cys Gln Glu Asn Gln Trp Leu Arg Asp Glu Leu Ala Gly Thr Gln Gln
75              115                 120                 125
76     Arg Leu Gln Arg Ser Glu Gln Ala Val Ala Gln Leu Glu Glu Glu Lys
77         130                 135                 140
78     Lys His Leu Glu Phe Leu Gly Gln Leu Arg Gln Tyr Asp Glu Asp Gly
79     145                 150                 155                 160
80     His Thr Ser Glu Glu Lys Glu Gly Asp Ala Thr Lys Asp Ser Leu Asp
81                 165                 170                 175
82     Asp Leu Phe Pro Asn Glu Glu Glu Glu Asp Pro Ser Asn Gly Leu Ser
83                 180                 185                 190
84     Arg Gly Gln Gly Ala Thr Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro
85         195                 200                 205
86     Ala Arg Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ala Gln
87         210                 215                 220
88     Gly Arg Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp
89     225                 230                 235                 240
90     Leu Glu Arg Thr Ser Gly Arg Gly His Pro Asp Val Ala Thr Met Leu
91                 245                 250                 255
92     Asn Ile Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala
93                 260                 265                 270
94     Ala His Leu Leu Asn Asp Ala Leu Ser Ile Arg Glu Ser Thr Leu Gly
95                 275                 280                 285
96     Pro Asp His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu
97         290                 295                 300
98     Tyr Gly Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Gln Arg
99     305                 310                 315                 320
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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/036,614A

INPUT SET: S30854.raw

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100        Ala Leu Glu Ile Arg Glu Lys Val Leu Gly Thr Asn His Pro Asp Val
101                        325             330                 335
102        Ala Lys Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys
103                        340             345                 350
104        Tyr Glu Ala Val Glu Arg Tyr Tyr Gln Arg Ala Leu Ala Ile Tyr Glu
105                        355             360                 365
106        Gly Gln Leu Gly Pro Asp Asn Pro Asn Val Ala Arg Thr Lys Asn Asn
107            370             375                 380
108        Leu Ala Ser Cys Tyr Leu Lys Gln Gly Lys Tyr Ala Glu Ala Glu Thr
109        385             390                 395                 400
110        Leu Tyr Lys Glu Ile Leu Thr Arg Ala His Val Gln Glu Phe Gly Ser
111                        405             410                 415
112        Val Asp Asp Asp His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu
113                        420             425                 430
114        Glu Met Ser Lys Ser Arg His His Glu Gly Gly Thr Pro Tyr Ala Glu
115                        435             440                 445
116        Tyr Gly Gly Trp Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn
117            450             455                 460
118        Thr Thr Leu Arg Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu
119        465             470                 475                 480
120        Glu Ala Ala Glu Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln
121                        485             490                 495
122        Gly Thr Asp Pro Ile Ser Gln Thr Lys Val Ala Glu Leu Leu Gly Glu
123                        500             505                 510
124        Ser Asp Gly Arg Arg Thr Ser Gln Glu Gly Pro Gly Asp Ser Val Lys
125            515             520                 525
126        Phe Glu Gly Gly Glu Asp Ala Ser Val Ala Val Glu Trp Ser Gly Asp
127            530             535                 540
128        Gly Ser Gly Thr Leu Gln Arg Ser Gly Ser Leu Gly Lys Ile Arg Asp
129        545             550                 555                 560
130        Val Leu Arg Arg Ser Ser Glu Leu Leu Val Arg Lys Leu Gln Gly Thr
131                        565             570                 575
132        Glu Pro Arg Pro Ser Ser Ser Asn Met Lys Arg Ala Ala Ser Leu Asn
133                        580             585                 590
134        Tyr Leu Asn Gln Pro Ser Ala Ala Pro Leu Gln Val Ser Arg Gly Leu
135            595             600                 605
136        Ser Ala Ser Thr Met Asp Leu Ser Ser Ser Ser
137            610             615
138
139            (2) INFORMATION FOR SEQ ID NO:2:
140
141            (i) SEQUENCE CHARACTERISTICS:
142                (A) LENGTH: 2453 base pairs
143                (B) TYPE: nucleic acid
144                (C) STRANDEDNESS: single
145                (D) TOPOLOGY: linear
146
147        (vii) IMMEDIATE SOURCE:
148                (A) LIBRARY: SMCANOT01
149                (B) CLONE: 2479739
150
151        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
152
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INPUT SET: S30854.raw

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153     GTGAAGTGGT GAAAGAAGGG GTGGGAACGC TGGACTTCTG GACTTTGGGC AGGGCAGATC      60
154     CTCTGACTCT CTGGCTGCAG AACAGTTTCT TCCGTGCTCT GGCCTGAGTG CCCACAGGCC     120
155     AGGGGCCTCT GCTCTGTACA CAGACCGGGC AAGGTCCCCC AGGCCAGGAT GTCAGGCCTG     180
156     GTGTTGGGGC AGCGGGATGA GCCTGCAGGC CACCGGCTCA GCCAAGAGGA GATCCTGGGG     240
157     AGCACACGGC TGGTCAGCCA AGGGCTAGAG GCCCTACGCA GTGAACACCA GGCCGTGCTG     300
158     CAAAGCCTGT CCCAGACCAT TGAGTGTCTG CAGCAGGGAG GCCATGAGGA AGGGCTGGTG     360
159     CATGAGAAGG CCCGGCAGCT TCGCCGTTCT ATGGAAAACA TTGAGCTCGG GCTGAGTGAG     420
160     GCCCAGGTGA TGCTGGCTCT AGCCAGCCAC CTGAGCACAG TGGAGTCGGA GAAACAGAAG     480
161     CTGCGGGCTC AGGTGCGGCG GCTATGCCAG GAGAACCAGT GGCTGCGGGA TGAGCTGGCT     540
162     GGCACCCAGC AGCGGCTACA GCGCAGTGAA CAGGCTGTGG CTCAGCTGGA GGAGGAAAAG     600
163     AAGCACCTGG AGTTCCTGGG GCAGCTGCGG CAGTATGATG AGGATGGACA TACCTCGGAG     660
164     GAGAAAGAAG GCGATGCCAC CAAGGATTCC CTGGATGACC TCTTTCCTAA TGAGGAGGAA     720
165     GAGGACCCCA GCAATGGCTT GTCCCGTGGT CAAGGTGCTA CAGCAGCTCA GCAGGGTGGA     780
166     TATGAGATCC CAGCAAGGTT GCGGACGTTG CACAACCTGG TGATCCAGTA CGCAGCCCAA     840
167     GGTCGCTATG AGGTGGCCGT GCCACTCTGT AAGCAGGCAC TAGAGGACCT GGAGCGCACA     900
168     TCAGGCCGTG GCCACCCTGA TGTCGCCACC ATGCTCAACA TCCTTGCTTT GGTGTATCGT     960
169     GACCAGAATA AGTATAAGGA AGCTGCCCAC CTGCTGAATG ATGCCCTTAG CATCCGGGAG    1020
170     AGCACCTTGG GACCTGACCA TCCTGCTGTG GCTGCCACAC TCAACAATTT GGCTGTGCTC    1080
171     TATGGCAAAA GGGGCAAGTA CAAGGAGGCA GAGCCTCTGT GCCAGCGGGC ACTGGAGATT    1140
172     CGAGAAAAGG TCCTGGGCAC GAATCATCCA GATGTGGCAA AACAGCTGAA CAACCTGGCC    1200
173     CTCTTGTGCC AAAACCAGGG CAAGTATGAG GCCGTGGAAC GCTACTACCA GCGAGCACTG    1260
174     GCCATCTACG AGGGGCAGCT GGGGCCGGAC AACCCTAATG TAGCCCGGAC CAAGAACAAC    1320
175     CTGGCTTCCT GTTACCTGAA ACAGGGCAAA TATGCTGAGG CTGAGACACT ATACAAAGAG    1380
176     ATCCTGACCC GTGCCCATGT ACAGGAGTTT GGGTCTGTGG ATGATGACCA CAAGCCCATC    1440
177     TGGATGCATG CAGAGGAGCG GGAGGAAATG AGCAAAAGCC GGCACCATGA GGGTGGGACA    1500
178     CCCTATGCTG AGTATGGAGG CTGGTACAAG GCCTGCAAAG TGAGCAGCCC CACAGTGAAC    1560
179     ACTACTCTGA GAAACCTGGG AGCTCTGTAT AGGCGCCAGG GAAAGCTGGA GGCTGCTGAG    1620
180     ACCCTGGAGG AATGTGCCCT GCGGTCCCGG AGACAGGGCA CTGACCCTAT CAGCCAGACG    1680
181     AAGGTGGCAG AGCTGCTTGG GGAGAGTGAT GGTAGAAGGA CCTCCCAGGA GGGCCCTGGA    1740
182     GACAGTGTGA AATTCGAGGG TGGTGAAGAT GCTTCTGTGG CTGTGGAGTG GTCCGGGGAT    1800
183     GGCAGTGGGA CCCTGCAGAG GAGTGGCTCT CTTGGCAAGA TCCGGGATGT GCTCCGCAGA    1860
184     AGCAGTGAAC TCTTGGTGAG GAAGCTCCAG GGGACTGAGC CTCGGCCCTC CAGCAGCAAC    1920
185     ATGAAGCGAG CAGCCTCCTT GAACTATCTG AACCAACCTA GTGCAGCACC CCTCCAGGTC    1980
186     TCCCGGGGCC TCAGTGCCAG CACCATGGAC CTCTCTTCAA GCAGCTGACA TTCAACCCGG    2040
187     CCCCCAGGTC TGCTGGGTCC CCCCACCCCC ACAGCCCTCA CAGCATTCCC CATTGCTCCT    2100
188     GGCTCTTCCC CACCCCTAGG TGGGACAGTG AAGGGGAGCA GTTTAACCAG AAGATTGCTG    2160
189     CTGCCCTTAG GGTCTCAGCT CCCTCCTCAG GAATCCCTCT TAGGAAGGAC CCTCAGGACA    2220
190     CCCTCTCTGC ACCCTGTGGT CCTCTAGAGT AGCTAGCTCT GAGGCCCCAA GGTGGGTACA    2280
191     AAGCAGGTAT GGCCCTCAGA GATGCAGCCT GCTGCTGGCT TTTCAGTCAG AGGGTTGGGG    2340
192     GCTGGCCAGC CAAGCTGCCT TGCCCTGGCC GCTCTTACTC CCTCCCTCTG CTGTCTCACT    2400
193     TCAGGTCCAT GTATTTCACT TTTCTTAAAT AAAAGAATCA GTNCTTNTNT NNG          2453
194
195                    (2) INFORMATION FOR SEQ ID NO:3:
196
197             (i) SEQUENCE CHARACTERISTICS:
198                 (A) LENGTH: 569 amino acids
199                 (B) TYPE: amino acid
200                 (C) STRANDEDNESS: single
201                 (D) TOPOLOGY: linear
202
203            (vii) IMMEDIATE SOURCE:
204                 (A) LIBRARY: GenBank
205                 (B) CLONE: 307085
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RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/036,614A*

INPUT SET: S30854.raw

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206
207          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
208
209     Met Ser Thr Met Val Tyr Ile Lys Glu Asp Lys Leu Glu Lys Leu Thr
210      1               5                  10                  15
211     Gln Asp Glu Ile Ile Ser Lys Thr Lys Gln Val Ile Gln Gly Leu Glu
212                  20                  25                  30
213     Ala Leu Lys Asn Glu His Asn Ser Ile Leu Gln Ser Leu Leu Glu Thr
214              35                  40                  45
215     Leu Lys Cys Leu Lys Lys Asp Asp Glu Ser Asn Leu Val Glu Glu Lys
216          50                  55                  60
217     Ser Asn Met Ile Arg Lys Ser Leu Glu Met Leu Glu Leu Gly Leu Ser
218      65                  70                  75                  80
219     Glu Ala Gln Val Met Met Ala Leu Ser Asn His Leu Asn Ala Val Glu
220                  85                  90                  95
221     Ser Glu Lys Gln Lys Leu Arg Ala Gln Val Arg Arg Leu Cys Gln Glu
222                 100                 105                 110
223     Asn Gln Trp Leu Arg Asp Glu Leu Ala Asn Thr Gln Gln Lys Leu Gln
224                 115                 120                 125
225     Lys Ser Glu Gln Ser Val Ala Gln Leu Glu Glu Glu Lys Lys His Leu
226                 130                 135                 140
227     Glu Phe Met Asn Gln Leu Lys Lys Tyr Asp Asp Asp Ile Ser Pro Ser
228                 145                 150                 155                 160
229     Glu Asp Lys Asp Thr Asp Ser Thr Lys Glu Pro Leu Asp Asp Leu Phe
230                 165                 170                 175
231     Pro Asn Asp Glu Asp Asp Pro Gly Gln Gly Ile Gln Gln Gln His Ser
232                 180                 185                 190
233     Ser Ala Ala Ala Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg
234                 195                 200                 205
235     Leu Arg Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ser Gln Gly Arg
236                 210                 215                 220
237     Tyr Glu Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu
238     225                 230                 235                 240
239     Lys Thr Ser Gly His Asp His Pro Asp Val Ala Thr Met Leu Asn Ile
240                 245                 250                 255
241     Leu Ala Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Asp Ala Ala Asn
242                 260                 265                 270
243     Leu Leu Asn Asp Ala Leu Ala Ile Arg Glu Lys Thr Leu Gly Lys Asp
244                 275                 280                 285
245     His Pro Ala Val Ala Ala Thr Leu Asn Asn Leu Ala Val Leu Tyr Gly
246                 290                 295                 300
247     Lys Arg Gly Lys Tyr Lys Glu Ala Glu Pro Leu Cys Lys Arg Ala Leu
248     305                 310                 315                 320
249     Glu Ile Arg Glu Lys Val Leu Gly Lys Asp His Pro Asp Val Ala Lys
250                 325                 330                 335
251     Gln Leu Asn Asn Leu Ala Leu Leu Cys Gln Asn Gln Gly Lys Tyr Glu
252                 340                 345                 350
253     Glu Val Glu Tyr Tyr Tyr Gln Arg Ala Leu Glu Ile Tyr Gln Thr Lys
254                 355                 360                 365
255     Leu Gly Pro Asp Asp Pro Asn Val Ala Lys Thr Lys Asn Asn Leu Ala
256                 370                 375                 380
257     Ser Cys Tyr Leu Lys Gln Gly Lys Phe Lys Gln Ala Glu Thr Leu Tyr
258     385                 390                 395                 400
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/036,614A*

DATE: 03/01/1999
TIME: 14:09:35

INPUT SET: S30854.raw

Line	Error	Original Text
30	Wrong application Serial Number	(A) APPLICATION NUMBER: To Be Assigned